

K. S. S. S. S.

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PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/878,177DATE: 03/29/1999
TIME: 13:54:01

Input Set: H878177.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Chugai Seiyaku Kabushiki Kaisha, 5001, Iwamoto et
2 <120> TITLE OF INVENTION: Cell Calcification Suppressing Proteins and Genes of
3 the Proteins
4 <130> FILE REFERENCE: chugai seiyaku kabushiki kaisha 5001
5 <140> CURRENT APPLICATION NUMBER: US/08/878,177
6 <141> CURRENT FILING DATE: 1997-06-18
7 <160> NUMBER OF SEQ ID NOS: 7
8 <170> SOFTWARE: PatentIn Ver. 2.0
9 <210> SEQ ID NO 1
10 <211> LENGTH: 1447
11 <212> TYPE: DNA
12 <213> ORGANISM: C-11 gene, c-erg gene w/ deletion, chicken DNA
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16 agtgtgccta cggatcgccc caccttgcaa agacagaaat gacagcctcc tcttcagtg 180
17 aatatgggca aacatcaaag atgagcccg cgcgttcccca gcaggactgg ttatcacagc 240
18 ccccgccag agttaccatt aagatggagt gtaacccaaa ccagggttaat ggggtcaagga 300
19 attcacctga tgactgcagc gtggcaaaaag gagggaaaat ggtagcagt tcagacaatg 360
20 ttgggatgaa ctatggaagc tacatggaag agaagcatat tccgcctcca aatatgacaa 420
21 ccaatgaacg aagagttatt gtgccagcag atcctacgtt atggagcaca gaccatgtac 480
22 ggagtggtgct ggagtgggca gtgaaggagt atggtcttcc agacgtggac atcttgttgt 540
23 tccagaacat tgatgggaaa gagttgtgta aaatgaccaa agatgacttc cagagactca 600
24 cgccgagcta taacgcagat atcctcctgt cacacctaca ctacctcaga gagagaggag 660
25 ccacttttat ttttccaaat acatcagttt acccagaagc aacgcaaaga ataacaacaa 720
26 ggccagattt accttatgag caagcgagga gatcagcgtg gacgagtcac agccatccca 780
27 ctacgtcaaa agctacccaa ccatcatctt caacagtgcc caaaacagaa gaccagcgtc 840
28 ctacgttaga tccttatcag attcttgagc cgaccagcag ccgtcttgca aatccaggga 900
29 gtgggcagat acagctatgg cagttcctac tggagcttct gtcggacagc tccaactcca 960
30 actgcatcac ctgggagggc acaaatgggg agttcaagat gacagaccct gatgaagtgg 1020
31 ctcggcgttg gggagagagg aaaagcaaac ctaacatgaa ctatgacaaa ctacagcgtg 1080
32 cacttcgcta ctactatgac aaaaatatta tgactaaagt tcatggtaaa cgctatgcct 1140
33 acaaatattga tttccacgga atcgctcagg ccctccagcc tcaccctcca gaatcatcca 1200
34 tgtacaaata cccatcagac ctcccctaca tgagttccta ccatgcacac cccagaaga 1260
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38 aagaaaa 1447
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41 <212> TYPE: PRT
42 <213> ORGANISM: protein sequence from C-11 gene
43 <400> SEQUENCE: 2
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PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/878,177

DATE: 03/29/1999
TIME: 13:54:01

Input Set: H878177.RAW

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50	Pro Arg Val Pro Gln Gln Asp Trp Leu Ser Gln Pro Pro Ala Arg Val			
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52	Thr Ile Lys Met Glu Cys Asn Pro Asn Gln Val Asn Gly Ser Arg Asn			
53		65	70	75
54	Ser Pro Asp Asp Cys Ser Val Ala Lys Gly Gly Lys Met Val Ser Ser			
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56	Ser Asp Asn Val Gly Met Asn Tyr Gly Ser Tyr Met Glu Glu Lys His			
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60	Ala Asp Pro Thr Leu Trp Ser Thr Asp His Val Arg Gln Trp Leu Glu			
61		130	135	140
62	Trp Ala Val Lys Glu Tyr Gly Leu Pro Asp Val Asp Ile Leu Leu Phe			
63		145	150	155
64	Gln Asn Ile Asp Gly Lys Glu Leu Cys Lys Met Thr Lys Asp Asp Phe			
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66	Gln Arg Leu Thr Pro Ser Tyr Asn Ala Asp Ile Leu Leu Ser His Leu			
67		180	185	190
68	His Tyr Leu Arg Glu Arg Gly Ala Thr Phe Ile Phe Pro Asn Thr Ser			
69		195	200	205
70	Val Tyr Pro Glu Ala Thr Gln Arg Ile Thr Thr Arg Pro Asp Leu Pro			
71		210	215	220
72	Tyr Glu Gln Ala Arg Arg Ser Ala Trp Thr Ser His Ser His Pro Thr			
73		225	230	235
74	Gln Ser Lys Ala Thr Gln Pro Ser Ser Ser Thr Val Pro Lys Thr Glu			
75		245	250	255
76	Asp Gln Arg Pro Gln Leu Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser			
77		260	265	270
78	Ser Arg Leu Ala Asn Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe			
79		275	280	285
80	Leu Leu Glu Leu Leu Ser Asp Ser Ser Asn Ser Asn Cys Ile Thr Trp			
81		290	295	300
82	Glu Gly Thr Asn Gly Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala			
83		305	310	315
84	Arg Arg Trp Gly Glu Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys			
85		325	330	335
86	Leu Ser Arg Ala Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys			
87		340	345	350
88	Val His Gly Lys Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala			
89		355	360	365
90	Gln Ala Leu Gln Pro His Pro Pro Glu Ser Ser Met Tyr Lys Tyr Pro			
91		370	375	380
92	Ser Asp Leu Pro Tyr Met Ser Ser Tyr His Ala His Pro Gln Lys Met			
93		385	390	395
94	Asn Phe Val Ala Pro His Pro Pro Ala Leu Pro Val Thr Ser Ser Ser			400

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/878,177

DATE: 03/29/1999
TIME: 13:54:01

Input Set: H878177.RAW

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95              405              410              415
96      Phe Phe Ala Ala Pro Asn Pro Tyr Trp Asn Ser Pro Thr Gly Gly Ile
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98      Tyr Pro Asn Thr Arg Leu Pro Ala Ala His Met Pro Ser His Leu Gly
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100     Thr Tyr Tyr
101              450
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108      ttatggcaag cactattaag gaagcattat cagtggtag tgaagaccag tccttgtttg 120
109      agtgtgccta cggatcgccc caccttgcaa agacagaaat gacagcctcc tcttcagtg 180
110      aatatgggca aacatcaaag atgagccgc gcgttcccca gcaggactgg ttatcacagc 240
111      ccccggccag agttaaccatt aagatggagt gtaacccaaa ccaggttaat ggggtcaagga 300
112      attcacctga tgactgcagc gtggcaaaag gagggaaaat ggtagcagt tcagacaatg 360
113      ttgggatgaa ctatggaagc tacatggaag agaagcatat tccgcctcca aatatgacaa 420
114      ccaatgaacg aagagttatt gtgccagcag atcctacgtt atggagcaca gaccatgtac 480
115      ggtagtggtt ggagtgggca gtgaaggagt atggtcttcc agacgtggac atcttgttgt 540
116      tccagaacat tgatgggaaa gagttgtgta aaatgaccaa agatgacttc cagagactca 600
117      cgccgagcta taacgcagat atcctcctgt cacacctaca ctacctcaga gagactcctc 660
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119      atgctagaaa cacaggagga gccactttta tttttccaaa tacatcagtt taccagaag 780
120      caacgcaaag aataacaaca aggccagatt taccttatga gcaagcgagg agatcagcgt 840
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126      actatgacaa actcagccgt gcacttcgct actactatga caaaaatatt atgactaaag 1200
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129      accatgcaca cccccagaag atgaactttg tagctcccca tccccctgct ttgcccgtaa 1380
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141      20              25              30
142      Met Thr Ala Ser Ser Ser Ser Glu Tyr Gly Gln Thr Ser Lys Met Ser
143      35              40              45
144      Pro Arg Val Pro Gln Gln Asp Trp Leu Ser Gln Pro Pro Ala Arg Val

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PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/878,177

DATE: 03/29/1999
TIME: 13:54:01

Input Set: H878177.RAW

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148	Ser	Pro	Asp	Asp	Cys	Ser	Val	Ala	Lys	Gly	Gly	Lys	Met	Val	Ser	Ser	
149					85					90						95	
150	Ser	Asp	Asn	Val	Gly	Met	Asn	Tyr	Gly	Ser	Tyr	Met	Glu	Glu	Lys	His	
151				100					105					110			
152	Ile	Pro	Pro	Pro	Asn	Met	Thr	Thr	Asn	Glu	Arg	Arg	Val	Ile	Val	Pro	
153				115					120					125			
154	Ala	Asp	Pro	Thr	Leu	Trp	Ser	Thr	Asp	His	Val	Arg	Gln	Trp	Leu	Glu	
155		130					135						140				
156	Trp	Ala	Val	Lys	Glu	Tyr	Gly	Leu	Pro	Asp	Val	Asp	Ile	Leu	Leu	Phe	
157	145					150					155					160	
158	Gln	Asn	Ile	Asp	Gly	Lys	Glu	Leu	Cys	Lys	Met	Thr	Lys	Asp	Asp	Phe	
159				165						170					175		
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161				180					185					190			
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163			195					200					205				
164	Asp	Lys	Ala	Leu	Gln	Asn	Ser	Pro	Arg	Leu	Met	His	Ala	Arg	Asn	Thr	
165		210					215					220					
166	Gly	Gly	Ala	Thr	Phe	Ile	Phe	Pro	Asn	Thr	Ser	Val	Tyr	Pro	Glu	Ala	
167	225					230					235					240	
168	Thr	Gln	Arg	Ile	Thr	Thr	Arg	Pro	Asp	Leu	Pro	Tyr	Glu	Gln	Ala	Arg	
169				245						250					255		
170	Arg	Ser	Ala	Trp	Thr	Ser	His	Ser	His	Pro	Thr	Gln	Ser	Lys	Ala	Thr	
171			260						265					270			
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173			275					280					285				
174	Leu	Asp	Pro	Tyr	Gln	Ile	Leu	Gly	Pro	Thr	Ser	Ser	Arg	Leu	Ala	Asn	
175		290					295					300					
176	Pro	Gly	Ser	Gly	Gln	Ile	Gln	Leu	Trp	Gln	Phe	Leu	Leu	Glu	Leu	Leu	
177	305					310					315					320	
178	Ser	Asp	Ser	Ser	Asn	Ser	Asn	Cys	Ile	Thr	Trp	Glu	Gly	Thr	Asn	Gly	
179				325						330					335		
180	Glu	Phe	Lys	Met	Thr	Asp	Pro	Asp	Glu	Val	Ala	Arg	Arg	Trp	Gly	Glu	
181			340						345					350			
182	Arg	Lys	Ser	Lys	Pro	Asn	Met	Asn	Tyr	Asp	Lys	Leu	Ser	Arg	Ala	Leu	
183			355					360						365			
184	Arg	Tyr	Tyr	Tyr	Asp	Lys	Asn	Ile	Met	Thr	Lys	Val	His	Pro	Pro	Glu	
185		370					375					380					
186	Ser	Ser	Met	Tyr	Lys	Tyr	Pro	Ser	Asp	Leu	Pro	Tyr	Met	Ser	Ser	Tyr	
187	385					390					395					400	
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189				405						410					415		
190	Ala	Leu	Gln	Pro	His	Ala	His	Pro	Gln	Lys	Met	Asn	Phe	Val	Ala	Pro	
191				420					425					430			
192	His	Pro	Pro	Ala	Leu	Pro	Val	Thr	Ser	Ser	Ser	Phe	Phe	Ala	Ala	Pro	
193			435					440					445				
194	Asn	Pro	Tyr	Trp	Asn	Ser	Pro	Thr	Gly	Gly	Ile	Tyr	Pro	Asn	Thr	Arg	

PAGE: 5

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/878,177DATE: 03/29/1999
TIME: 13:54:01

Input Set: H878177.RAW

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PAGE: 6

VERIFICATION SUMMARY
PATENT APPLICATION US/08/878,177

DATE: 03/29/1999
TIME: 13:54:01

Input Set: H878177.RAW

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